

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 14:04:54 ; Search time 1 Seconds

(without alignments)  
6.964 Million cell updates/sec

Title: us-09-944-896-49

Perfect score: 1876

Sequence: 1 ctctttgtccaccagccca.....tcagctgaaaaaaaaa 1876

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 1856 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : seq264-1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1764.5	94.1	1856	1	us-09-790-264-1
2	25.8	1.4	1856	1	us-09-790-264-1

ALIGNMENTS

RESULT 1  
us-09-790-264-1

Query Match 94.1% Score 1764.5; DB 1; Length 1856;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

QY	46	GCTCCATCCAGCCCTGAGAAACAGCCGGGTGGCTGAGCCAGGCTGTGCAGGAGACCTG	105
DB	18	GCTCCATCCAGCCCTGAGAAACAGCCGGGTGGCTGAGCCAGGCTGTGCAGGAGACCTG	77
QY	106	ACGGGCCCCAAGACCCATGCTGATCCAGAGACCTCCCTGGCCGGGGGACATCTCTGG	165
DB	78	ACGGGCCCCAAGACCCATGCTGATCCAGAGACCTCCCTGGCCGGGGGACATCTCTGG	137
QY	166	CTGTCCTCTGGCCCTCTCTGGGACACCTGGGAGAGAGGTGTGGCCACCCCACTGAGG	225
DB	138	CTGTCCTCTGGCCCTCTCTGGGACACCTGGGAGAGAGGTGTGGCCACCCCACTGAGG	197
QY	226	AGCAGGCTCCGATGGCCGAGCCCTGAAACAGAGAGAGATTTCTTCTCTCCCTG	285
DB	198	AGCAGGCTCCGATGGCCGAGCCCTGAAACAGAGAGAGATTTCTTCTCTCCCTG	257
QY	286	ACAAACGCTGCGAGCTGGGTCCAGCCCTCGGAGCTGACATGCGAGGCTGAGTGA	345
DB	258	ACAAACGCTGCGAGCTGGGTCCAGCCCTCGGAGCTGACATGCGAGGCTGAGTGA	317

Sequence Alignment

QY	346	GTGACAGCTGGCCCAACTGCTCAAGCCAGGGAGCCCTGTGGAAATCCAAACCCGA	405
DB	318	GTGACAGCTGGCCCAACTGCTCAAGCCAGGGAGCCCTGTGGAAATCCAAACCCGA	377
QY	406	GCTTGGATCCGCTGTGGCCGACCCCTGCAAGTGGCTGGAACATGACTGCTGCCG	465
DB	378	GCTTGGATCCGCTGTGGCCGACCCCTGCAAGTGGCTGGAACATGACTGCTGCCG	437
QY	466	CGGCTTGGGCTCTTTGTTGAAGTGTACACCTATGTTTGGAGAGGGGACGGGTACA	525
DB	438	CGGCTTGGGCTCTTTGTTGAAGTGTACACCTATGTTTGGAGAGGGGACGGGTACA	497
QY	526	GCCACGGGAGAGAGTGTGCTCGAAGCCCACTGCAACCCACTACAGAGCTGTGT	585
DB	498	GCCACGGGAGAGAGTGTGCTCGAAGCCCACTGCAACCCACTACAGAGCTGTGT	557
QY	586	GGGCAACCTCAAGCCAGCTGGGCTGTGGCCGACCTGTGCTGCAAGGACAGACGA	645
DB	558	GGGCAACCTCAAGCCAGCTGGGCTGTGGCCGACCTGTGCTGCAAGGACAGACGA	617
QY	646	TAGAACCTTTGTCTGTGCTTACTCCCGAGAGCACTGGAGGTCAACGGGAGACAA	705
DB	618	TAGAACCTTTGTCTGTGCTTACTCCCGAGAGCACTGGAGGTCAACGGGAGACAA	677
QY	706	TCATCCCTATAGAAGGGTGGCTGTGCTGTGCTGTGCAAGCCAGTGTAGGCTGT	765
DB	678	TCATCCCTATAGAAGGGTGGCTGTGCTGTGCTGTGCAAGCCAGTGTAGGCTGT	737
QY	766	TCAAAGCTTGGGACATGAGGGGCTGTGAGGTGCCAGGAATCCTTGGCATGA	825
DB	738	TCAAAGCTTGGGACATGAGGGGCTGTGAGGTGCCAGGAATCCTTGGCATGA	797
QY	826	GCTGCCAAGAACATGAGCTGTCAACATCAGACCTGCACTGCTCCCTGCTGCT	885
DB	798	GCTGCCAAGAACATGAGCTGTCAACATCAGACCTGCACTGCTCCCTGCTGCT	857
QY	886	ACACGGGAGATATCTGACCAAGTGTGAGCTGACCTGATGTGTGCAAGGCGGCTCGG	945
DB	858	ACACGGGAGATATCTGACCAAGTGTGAGCTGACCTGATGTGTGCAAGGCGGCTCGG	917
QY	946	AGAGAGAGTGTGCTGCTGTGACATGAGCTGTGAGGGGAGCCCAAGTGTGCCACCAAG	1005
DB	918	AGAGAGAGTGTGCTGCTGTGACATGAGCTGTGAGGGGAGCCCAAGTGTGCCACCAAG	977
QY	1006	TGCAATTTCTTCCACACACTGTGACCTGAGAGTGTGAGGAGTGTGATGATGTCTT	1065
DB	978	TGCAATTTCTTCCACACACTGTGACCTGAGAGTGTGAGGAGTGTGATGATGTCTT	1037
QY	1066	CAGAGGACAGACCTTATACAGAGCCAGAGTAAATGTACAGAAAGGCGGGGTCTGG	1125
DB	1038	CAGAGGACAGACCTTATACAGAGCCAGAGTAAATGTACAGAAAGGCGGGGTCTGG	1097
QY	1126	CCAGATCAAGAGCCAGAAAGTGCAGAGATCTCTGCTTCTATCTGGGCGGCTGGAGA	1185
DB	1098	CCAGATCAAGAGCCAGAAAGTGCAGAGATCTCTGCTTCTATCTGGGCGGCTGGAGA	1157
QY	1186	CCACCAAGAGTGTGACATGACCTGAGAGACCAAGAACTTGTGGGCTCCACT	1245
DB	1158	CCACCAAGAGTGTGACATGACCTGAGAGACCAAGAACTTGTGGGCTCCACT	1217
QY	1246	ACAAGACGCAAGAGACTCTTCCGCTGGGCAACAGGGAGACCAAGGCTTCAACAGTT	1305
DB	1218	ACAAGACGCAAGAGACTCTTCCGCTGGGCAACAGGGAGACCAAGGCTTCAACAGTT	1277
QY	1306	TTGCTTTGGGAGGCTTATCAACACAGGCTGTGTGCTGAGTCTCCATGGGGTTTG	1365
DB	1278	TTGCTTTGGGAGGCTTATCAACACAGGCTGTGTGCTGAGTCTCCATGGGGTTTG	1340
QY	1366	GCAACTGGTGGAGCTGAGGCTTCAAGTGTGCTTCAACTGGAAGACAGGCTGCAAAA	1425
DB	1341	GCAACTGGTGGAGCTGAGGCTTCAAGTGTGCTTCAACTGGAAGACAGGCTGCAAAA	1370

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# OM protein - protein search, using sw model

Run on: September 17, 2003, 14:00:33 ; Search time 0.001 seconds  
(without alignments)  
202.930 Million cell updates/sec

Title: us-09-944-896-50

Perfect score: 2529  
Sequence: 1 MHPTSPGRGHLLAVLLAL.....RNRYICOPQOEHSRWPGS 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 446 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : seq264-2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2447.5	96.8	446	1	us-09-790-264-2

## ALIGNMENTS

RESULT 1  
us-09-790-264-2

Query Match 96.8%; Score 2447.5; DB 1; Length 446;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 442; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY	DB	Sequence	Score	Length	ID	Description
QY	1	MHPTSPGRGHLLAVLLALIGTWAQVWPOLQOAPWAGALNRKESFLISLHNRIRS 60				
DB	1	MHPTSPGRGHLLAVLLALIGTWAQVWPOLQOAPWAGALNRKESFLISLHNRIRS 60				
QY	61	WYQPPAADRRRLDMSDSLQALQARALCGIPTPSLASGLWRTLOVGNMOLLPLGLASF 120				
DB	61	WYQPPAADRRRLDMSDSLQALQARALCGIPTPSLASGLWRTLOVGNMOLLPLGLASF 120				
QY	121	VEVVSIMFPAEGQRYSHAGECARNATCTHYTQLVWATSSQLCGRHLCASAGTALFAVC 180				
DB	121	VEVVSIMFPAEGQRYSHAGECARNATCTHYTQLVWATSSQLCGRHLCASAGTALFAVC 180				
QY	181	AYSPGNNVEVNTKTIIPYKKGAWCSICTASVSGCKAMDHAGLCEVPRNCRMSQNHG 240				
DB	181	AYSPGNNVEVNTKTIIPYKKGAWCSICTASVSGCKAMDHAGLCEVPRNCRMSQNHG 240				
QY	241	RLNISTCHCHCPGYTGRCYRCSLQCVHGRFREECSCVCDIGYGAGCATKYHFPFH 300				
DB	241	RLNISTCHCHCPGYTGRCYRCSLQCVHGRFREECSCVCDIGYGAGCATKYHFPFH 300				

QY	DB	Sequence	Score	Length	ID	Description
QY	301	TCDLRIDGCFWVSSSEADTYRRAMKQRRKGGVLAQIKSOKVODILAFYLGRLTTEVT 360				
DB	301	TCDLRIDGCFWVSSSEADTYRRAMKQRRKGGVLAQIKSOKVODILAFYLGRLTTEVT 360				
QY	361	DSDFETNFWIGLTYKAKDSFRWATGEHQAFSPAFGQPDNGLWLSAAMFGNVEL 420				
DB	361	DSDFETNFWIGLTYKAKDSFRWATGEHQAFSPAFGQPDNGLWLSAAMFGNVEL 420				
QY	421	QASAFNWNDOCKTRNRRTICOPQOEHSRWPGS 455				
DB	412	QASAFNWNDOCKTRNRRTICOPQOEHSRWPGS 446				

Search completed: September 17, 2003, 14:00:33  
Job time : 0.001 secs